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Investigating nano particles in bioinformatic analysis of the brucella genome for indication and differentation by qPCR

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Abstract

© 2016 Authors. Based on the identified genes, the design of specific primers and probes for qPCR was made, which makes it possible to differentiate B. melitensis and B. abortus in a single reaction. For the differentiation of Brucella strains of the same species, the PCR method of multilocus VNTR analysis, optimized for uniform temperature conditions, is described. In addition, MLVA profiles for B. abortus and B. melitensis genomes are presented. All methods of indication and differentiation of Brucella species and strains are described in detail, which allows them to be used in the everyday work of any PCR laboratory dealing with brucellosis. Control of amplification in the indication of bacteria of the genus Brucella and determination of their belonging to B. abortus and B. melitensis species is recommended to be carried out using the plasmid DNA designed in this work.

Keywords

Brucella, Genome, Identification, Indication;nano particle, MLVA, QPCR

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